

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/543,122
Source: DC
Date Processed by STIC: 6/14/06

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IAP7 Rec'd PCT/PTO 20 JUN 2006'



PCT

RAW SEQUENCE LISTING

DATE: 06/14/2006

PATENT APPLICATION: US/10/543,122

TIME: 10:29:10

Input Set : A:\186563-US-2.ST25.txt

Output Set: N:\CRF4\06142006\J543122.raw

3 <110> APPLICANT: Shenoy, Sudha
 4 Lefkowitz, Robert J.
 6 <120> TITLE OF INVENTION: Modified Trafficking Patterns for Arrestin and G-Protein-
 Coupled
 7 Receptors via Arrestin-Ubiquitin Chimera
 9 <130> FILE REFERENCE: 186563/US/2 (469390-00352)
 11 <140> CURRENT APPLICATION NUMBER: US 10/543,122
 C--> 12 <141> CURRENT FILING DATE: 2005-07-21
 14 <150> PRIOR APPLICATION NUMBER: US 60/442,403
 15 <151> PRIOR FILING DATE: 2003-01-24
 17 <160> NUMBER OF SEQ ID NOS: 45
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1581
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Synthetic
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1575)
 34 <400> SEQUENCE: 1
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 37 1 5 10 15
 39 ctg tac aag tcc gga ctc aga tct cga gct caa gct tcg aat tct gca 96
 40 Leu Tyr Lys Ser Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala
 41 20 25 30
 43 gtc gac ggt acc acg cgc acc atg ggt gaa aaa ccc ggg acc agg gtc 144
 44 Val Asp Gly Thr Thr Arg Thr Met Gly Glu Lys Pro Gly Thr Arg Val
 45 35 40 45
 47 ttc aag aag tcg agc cct aac tgc aag ctc acc gtg tac ttg ggc aag 192
 48 Phe Lys Lys Ser Ser Pro Asn Cys Lys Leu Thr Val Tyr Leu Gly Lys
 49 50 55 60
 51 cgt gac ttt gtg gat cac ttg gac aaa gtg gat cct gtc gat ggt gtg 240
 52 Arg Asp Phe Val Asp His Leu Asp Lys Val Asp Pro Val Asp Gly Val
 53 65 70 75 80
 55 gtg ctt gtg gat cct gac tac ttg aag gac cgg aaa gtg ttt gtg acc 288
 56 Val Leu Val Asp Pro Asp Tyr Leu Lys Asp Arg Lys Val Phe Val Thr
 57 85 90 95
 59 ctc acc tgt gcc ttc cgc tat ggc cga gaa gac ctg gat gta ctg ggc 336
 60 Leu Thr Cys Ala Phe Arg Tyr Gly Arg Glu Asp Leu Asp Val Leu Gly
 61 100 105 110
 63 ctg tct ttc cgc aaa gat ctg ttc atc gcc acc tac cag gcc ttc ccc 384

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64 Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
65      115      120      125
67 ccc atg ccc aac cca cct cgg ccc ccc acc cgc cta cag gac cga ctg      432
68 Pro Met Pro Asn Pro Pro Arg Pro Pro Thr Arg Leu Gln Asp Arg Leu
69      130      135      140
71 ctg aag aag ttg ggc cag cat gcc cac ccc ttt ttt ttc aca ata ccc      480
72 Leu Lys Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Ile Pro
73 145      150      155      160
75 cag aat ttg cct tgc tcc gtc aca ctg cag cca gga ccg gag gac aca      528
76 Gln Asn Leu Pro Cys Ser Val Thr Leu Gln Pro Gly Pro Glu Asp Thr
77      165      170      175
79 ggg aag gcc tgt gga gta gac ttt gag att cga gcc ttc tgt gcc aaa      576
80 Gly Lys Ala Cys Gly Val Asp Phe Glu Ile Arg Ala Phe Cys Ala Lys
81      180      185      190
83 tct ata gaa gaa aaa agc cac aaa agg aac tcc gtg cgg ctt atc atc      624
84 Ser Ile Glu Glu Lys Ser His Lys Arg Asn Ser Val Arg Leu Ile Ile
85      195      200      205
87 aga aag gta cag ttt gct cct gag aca ccc ggc ccc cag cca tca gct      672
88 Arg Lys Val Gln Phe Ala Pro Glu Thr Pro Gly Pro Gln Pro Ser Ala
89      210      215      220
91 gaa acc aca cgc cac ttc ctc atg tct gac cgg agg tcc ctg cac cta      720
92 Glu Thr Thr Arg His Phe Leu Met Ser Asp Arg Arg Ser Leu His Leu
93 225      230      235      240
95 gag gct tcc ctg gac aaa gag ctg tac tac cat ggg gaa ccc ctc aat      768
96 Glu Ala Ser Leu Asp Lys Glu Leu Tyr Tyr His Gly Glu Pro Leu Asn
97      245      250      255
99 gtc aac gtc cac gtc acc aac aat tct gcc aag acc gtc aag aag atc      816
100 Val Asn Val His Val Thr Asn Asn Ser Ala Lys Thr Val Lys Lys Ile
101      260      265      270
103 aga gtg tct gtg aga cag tat gcc gac att tgc ctc ttc agc acc gcg      864
104 Arg Val Ser Val Arg Gln Tyr Ala Asp Ile Cys Leu Phe Ser Thr Ala
105      275      280      285
107 cag tac aag tgt cct gtg gct cag ctt gaa caa gat gac cag gtg tct      912
108 Gln Tyr Lys Cys Pro Val Ala Gln Leu Glu Gln Asp Asp Gln Val Ser
109      290      295      300
111 ccc agt tcc aca ttc tgc aag gtg tac acc ata acc ccg ctg ctc agt      960
112 Pro Ser Ser Thr Phe Cys Lys Val Tyr Thr Ile Thr Pro Leu Leu Ser
113 305      310      315      320
115 gac aac cca gag aag cgt ggc ctt gcc ctt gat ggg caa ctc aag cac      1008
116 Asp Asn Pro Glu Lys Arg Gly Leu Ala Leu Asp Gly Gln Leu Lys His
117      325      330      335
119 caa gac acc aac ctg gct tcc agc acc att gtg aag gag gga gcc aac      1056
120 Gln Asp Thr Asn Leu Ala Ser Ser Thr Ile Val Lys Glu Gly Ala Asn
121      340      345      350
123 aag gag gtg ctg gga atc cta gta tcc tac agg gtc aac gtg aag ctg      1104
124 Lys Glu Val Leu Gly Ile Leu Val Ser Tyr Arg Val Asn Val Lys Leu
125      355      360      365
127 gtg gtg tct cca ggc ggc gat gtc tcc gtg gag cta cct ttc gtc cta      1152
128 Val Val Ser Pro Gly Gly Asp Val Ser Val Glu Leu Pro Phe Val Leu

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129      370      375      380
131 atg cac ccc aag ccc cac gac cac atc acc ctt ccc cga ccc cag tca      1200
132 Met His Pro Lys Pro His Asp His Ile Thr Leu Pro Arg Pro Gln Ser
133 385      390      395      400
135 gcc ccc cgg gaa ata gac atc cct gtg gat acc aac ctc att gaa ttc      1248
136 Ala Pro Arg Glu Ile Asp Ile Pro Val Asp Thr Asn Leu Ile Glu Phe
137      405      410      415
139 gat acc aac tat gcc aca gac gac gac atc gtg ttt gag gac ttt gcg      1296
140 Asp Thr Asn Tyr Ala Thr Asp Asp Asp Ile Val Phe Glu Asp Phe Ala
141      420      425      430
143 agg ctt cgg ctg aag ggg atg aag gat gac gac tgt gat gac cag ttc      1344
144 Arg Leu Arg Leu Lys Gly Met Lys Asp Asp Asp Cys Asp Asp Gln Phe
145      435      440      445
147 tgc gtc gac cag atc ttc gtg aag act ctg act ggt aag acc atc acc      1392
148 Cys Val Asp Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
149      450      455      460
151 ctc gag gtg gag ccc agt gac acc atc gag aat gtc aag gca aag atc      1440
152 Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile
153 465      470      475      480
155 caa gat aag gaa ggc att cct cct gat cag cag agg ttg atc ttt gcc      1488
156 Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
157      485      490      495
159 gga aaa cag ctg gaa gat ggt cgt acc ctg tct gac tac aac atc cag      1536
160 Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln
161      500      505      510
163 aaa gag tcc acc ttg cac ctg gta ctc cgt ctc aga ggt gggtga      1581
164 Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly
165      515      520      525
168 <210> SEQ ID NO: 2
169 <211> LENGTH: 525
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Synthetic Construct
176 <400> SEQUENCE: 2
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182 Leu Tyr Lys Ser Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala
183      20      25      30
186 Val Asp Gly Thr Thr Arg Thr Met Gly Glu Lys Pro Gly Thr Arg Val
187      35      40      45
190 Phe Lys Lys Ser Ser Pro Asn Cys Lys Leu Thr Val Tyr Leu Gly Lys
191      50      55      60
194 Arg Asp Phe Val Asp His Leu Asp Lys Val Asp Pro Val Asp Gly Val
195 65      70      75      80
198 Val Leu Val Asp Pro Asp Tyr Leu Lys Asp Arg Lys Val Phe Val Thr
199      85      90      95
202 Leu Thr Cys Ala Phe Arg Tyr Gly Arg Glu Asp Leu Asp Val Leu Gly
203      100      105      110

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206 Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
207      115      120      125
210 Pro Met Pro Asn Pro Pro Arg Pro Pro Thr Arg Leu Gln Asp Arg Leu
211      130      135      140
214 Leu Lys Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Ile Pro
215 145      150      155      160
218 Gln Asn Leu Pro Cys Ser Val Thr Leu Gln Pro Gly Pro Glu Asp Thr
219      165      170      175
222 Gly Lys Ala Cys Gly Val Asp Phe Glu Ile Arg Ala Phe Cys Ala Lys
223      180      185      190
226 Ser Ile Glu Glu Lys Ser His Lys Arg Asn Ser Val Arg Leu Ile Ile
227      195      200      205
230 Arg Lys Val Gln Phe Ala Pro Glu Thr Pro Gly Pro Gln Pro Ser Ala
231      210      215      220
234 Glu Thr Thr Arg His Phe Leu Met Ser Asp Arg Arg Ser Leu His Leu
235 225      230      235      240
238 Glu Ala Ser Leu Asp Lys Glu Leu Tyr Tyr His Gly Glu Pro Leu Asn
239      245      250      255
242 Val Asn Val His Val Thr Asn Asn Ser Ala Lys Thr Val Lys Lys Ile
243      260      265      270
246 Arg Val Ser Val Arg Gln Tyr Ala Asp Ile Cys Leu Phe Ser Thr Ala
247      275      280      285
250 Gln Tyr Lys Cys Pro Val Ala Gln Leu Glu Gln Asp Asp Gln Val Ser
251      290      295      300
254 Pro Ser Ser Thr Phe Cys Lys Val Tyr Thr Ile Thr Pro Leu Leu Ser
255 305      310      315      320
258 Asp Asn Pro Glu Lys Arg Gly Leu Ala Leu Asp Gly Gln Leu Lys His
259      325      330      335
262 Gln Asp Thr Asn Leu Ala Ser Ser Thr Ile Val Lys Glu Gly Ala Asn
263      340      345      350
266 Lys Glu Val Leu Gly Ile Leu Val Ser Tyr Arg Val Asn Val Lys Leu
267      355      360      365
270 Val Val Ser Pro Gly Gly Asp Val Ser Val Glu Leu Pro Phe Val Leu
271      370      375      380
274 Met His Pro Lys Pro His Asp His Ile Thr Leu Pro Arg Pro Gln Ser
275 385      390      395      400
278 Ala Pro Arg Glu Ile Asp Ile Pro Val Asp Thr Asn Leu Ile Glu Phe
279      405      410      415
282 Asp Thr Asn Tyr Ala Thr Asp Asp Asp Ile Val Phe Glu Asp Phe Ala
283      420      425      430
286 Arg Leu Arg Leu Lys Gly Met Lys Asp Asp Asp Cys Asp Asp Gln Phe
287      435      440      445
290 Cys Val Asp Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
291      450      455      460
294 Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile
295 465      470      475      480
298 Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
299      485      490      495
302 Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln

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303          500          505          510
306 Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly
307          515          520          525
310 <210> SEQ ID NO: 3
311 <211> LENGTH: 1581
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Synthetic
319 <220> FEATURE:
320 <221> NAME/KEY: CDS
321 <222> LOCATION: (1)..(1581)
323 <400> SEQUENCE: 3
324 ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag      48
325 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
326 1          5          10          15
328 ctg tac aag tcc gga ctc aga tct cga gct caa gct tcg aat tct gca      96
329 Leu Tyr Lys Ser Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala
330          20          25          30
332 gtc gac ggt acc acg cgc acc atg ggt gaa aaa ccc ggg acc agg gtc      144
333 Val Asp Gly Thr Thr Arg Thr Met Gly Glu Lys Pro Gly Thr Arg Val
334          35          40          45
336 ttc aag aag tcg agc cct aac tgc aag ctc acc gtg tac ttg ggc aag      192
337 Phe Lys Lys Ser Ser Pro Asn Cys Lys Leu Thr Val Tyr Leu Gly Lys
338          50          55          60
340 cgt gac ttt gtg gat cac ttg gac aaa gtg gat cct gtc gat ggt gtg      240
341 Arg Asp Phe Val Asp His Leu Asp Lys Val Asp Pro Val Asp Gly Val
342 65          70          75          80
344 gtg ctt gtg gat cct gac tac ttg aag gac cgg aaa gtg ttt gtg acc      288
345 Val Leu Val Asp Pro Asp Tyr Leu Lys Asp Arg Lys Val Phe Val Thr
346          85          90          95
348 ctc acc tgt gcc ttc cgc tat ggc cga gaa gac ctg gat gta ctg ggc      336
349 Leu Thr Cys Ala Phe Arg Tyr Gly Arg Glu Asp Leu Asp Val Leu Gly
350          100          105          110
352 ctg tct ttc cgc aaa gat ctg ttc atc gcc acc tac cag gcc ttc ccc      384
353 Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
354          115          120          125
356 ccc atg ccc aac cca cct cgg ccc ccc acc cgc cta cag gac cga ctg      432
357 Pro Met Pro Asn Pro Pro Arg Pro Pro Thr Arg Leu Gln Asp Arg Leu
358          130          135          140
360 ctg aag aag ttg ggc cag cat gcc cac ccc ttt ttt ttc aca ata ccc      480
361 Leu Lys Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Ile Pro
362 145          150          155          160
364 cag aat ttg cct tgc tcc gtc aca ctg cag cca gca ccg gag gac aca      528
365 Gln Asn Leu Pro Cys Ser Val Thr Leu Gln Pro Ala Pro Glu Asp Thr
366          165          170          175
368 ggg aag gcc tgt gga gta gac ttt gag att cga gcc ttc tgt gcc aaa      576
369 Gly Lys Ala Cys Gly Val Asp Phe Glu Ile Arg Ala Phe Cys Ala Lys
370          180          185          190

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : A:\186563-US-2.ST25.txt

Output Set: N:\CRF4\06142006\J543122.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6

VERIFICATION SUMMARY

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TIME: 10:29:11

Input Set : A:\186563-US-2.ST25.txt

Output Set: N:\CRF4\06142006\J543122.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date